

FIG. 1A

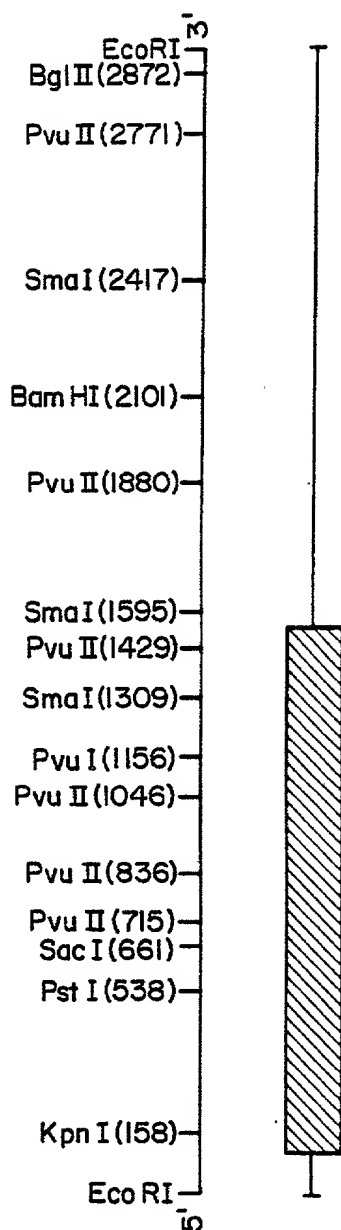


FIG. 1B-I

1 GCCATCTGGGCCAGGCCCATGCCCGAGGAGGGTGGTCTGAAGCCACAGAGCCCTGCCAGACTGCTGCCTCCCTTCTGACTG
 11
 21
 91 TGGCGGCTTGCCATGGCCAGCAACAGCAGCTCTGCCGACACCTGGGGGGGGCACCTCAATGGGTACCCGGTGCCCTACGCTTC
 31
 51
 181 PhePheProMetLeuGlyLeuSerProGlyAlaLeuThrThrLeuGlnHisGlnLeuProValSerGlyTyrSerThrPro
 61
 71
 271 SerProAlaThrIleGluThrGlnSerSerSerGluGluIleValProSerProProSerProProLeuProArgIleTyrLys
 TCCCCAGCCACCATTGAGACCCAGAGCAGAGTCTGAAGAGATAGTCCAGCCCTCCCTGCCACCCCTCTACCCGCGCATCTACAAG

FIG. 1B-2

91 101 111
 ProCysPheValCysGlnAspLysSerSerGlyTyrHisTyrGlyValSerAlaCysGluGlyCysLysGlyPhePheArgArgSerIle
 361 CCTTGGCTTGTCTGTCAGGACAAGTCTCAGGCTACCACTATGGGTACGGCTGTGAGGGCTGCAAGGGCTTCTTCGGCGCAGCATC
 121 131 141
 GlnLysAsnMetValTyrThrCysHisArgAspLysAsnCysIleIleAsnLysValThrArgAsnArgCysGlnTyrCysArgLeuGln
 451 CAGAAGAACATGGTGTACACGTGTACCGGGACAAGAACTGCATCATCAACAGGTGACCCGGAACCGCTGCCAGTACTGCCGACTGCAG
 151 161 171
 LysCysPheGluValGlyMetSerLysGluSerValArgAsnAspArgAsnLysLysLysGluValProLysProGluCysSerGlu
 541 AAGTGGCTTGAAGTGGCATGTCCAAGGAGTCTGTGAGAAACGACCGAAACAAGAGAAGAGGAGGTGCCAAGCCCGAGTGCCTCTGAG
 181 191 201
 SerTyrThrLeuThrProGluValGlyGluLeuIleGluLysValArgLysAlaHisGlnGluThrPheProAlaLeuCysGlnLeuGly
 631 AGCTACACGCTGACCGCGGAGGTGGGGAGCTCATTGAGAAGTGGCAAGGCAAGCCACCAAGAAACCTTCCCTGCCCTCTGCCAGCTGGGC
 211 221 231
 LysTyrThrThrAsnAsnSerSerGluGlnArgValSerLeuAspIleAspLeuTrpAspLysPheSerGluLeuSerThrLysCysIle
 721 AAATACACTACGAACAACAGCTCAGAACACGTGTCTCTGACATTGACCTCTGGGACAAGTTCACTGAACTCTCCACCAAGTGCATC
 241 251 261
 IleLysThrValGluPheAlaLysGlnLeuProGlyPheThrThrLeuThrIleAlaAspGlnIleThrLeuLeuLysAlaAlaCysLeu
 811 ATTAAGACTGTGGAGTTGCCCAAGCAGCTGCCCGCTTACCACCCCTCACCATTGCCGACCCAGATCACCTCCTCAAGGCTGCCTGCCTG
 271 281 291
 AspIleLeuIleLeuArgIleCysThrArgTyrThrProGluGlnAspThrMetThrPheSerAspGlyLeuThrLeuAsnArgThrGln
 901 GACATCCTGATCCTGCGGATCTGCACGCGGTACACGCCCGAGCAGGACACCATGACCTTCTCGGACGGCTGACCTTGAACCGGACCCAG
 301 311 321
 MethIleAsnAlaGlyPheGlyProLeuThrAspLeuValPheAlaPheAlaAsnGlnLeuLeuProLeuGluMetAspAspAlaGluThr
 991 ATGCACAACGCTGGCTTCGGCCCCCTCACCGACCTGGTCTTTGCCCTTCGCCAACCCAGCTGCTGCCCTGGAGATGGATGATGCCGGAGACG
 331 341 351
 GlyLeuLeuSerAlaIleCysLeuIleCysGlyAspArgGlnAspLeuGluGlnProAspArgValAspMetLeuGlnGluProLeuLeu
 1081 GGGCTGCTCAGCGCCATCTGCCCTCATCTGCGGGAGACCGCACCTGGAGCAGCCGCGGGTGGACATGCTGCAGGAGCCCGCTGCTG

FIG. 2A

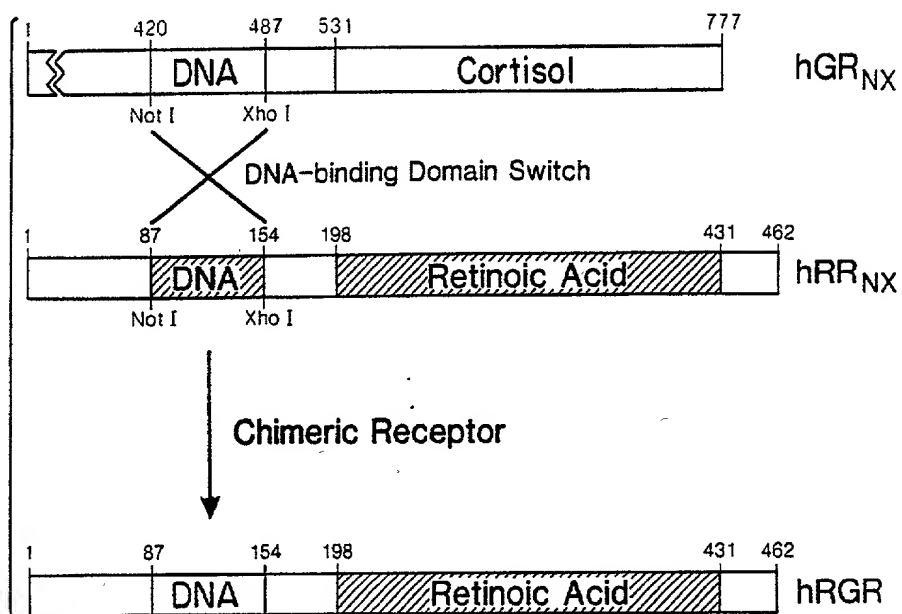
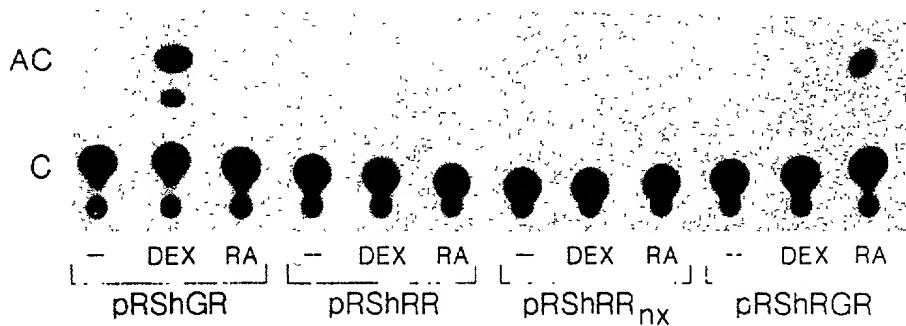


FIG. 2B



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FIG. 3A

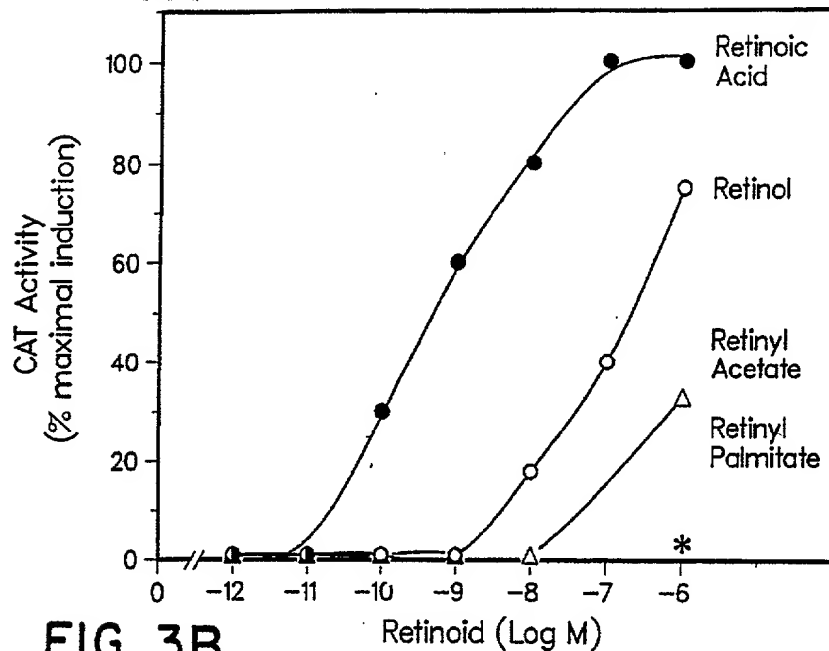


FIG. 3B

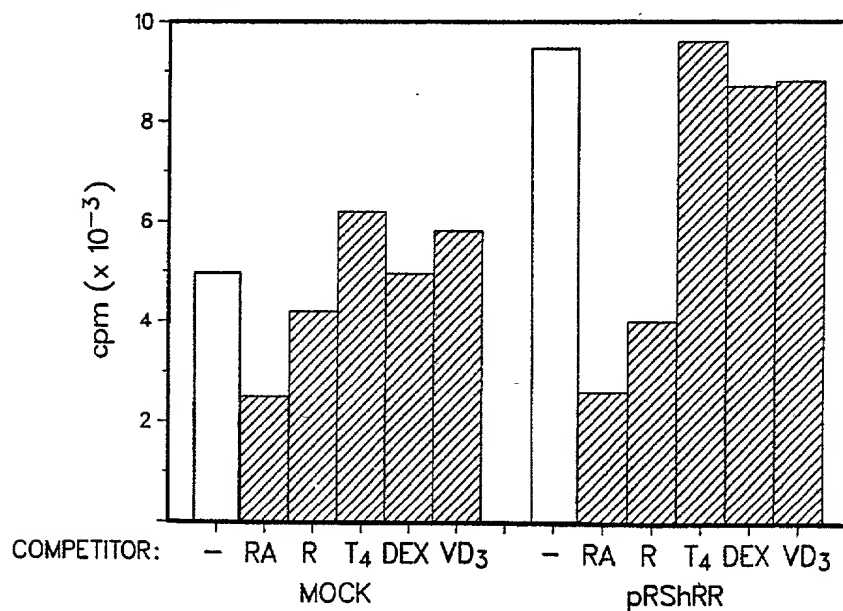


FIG. 4A

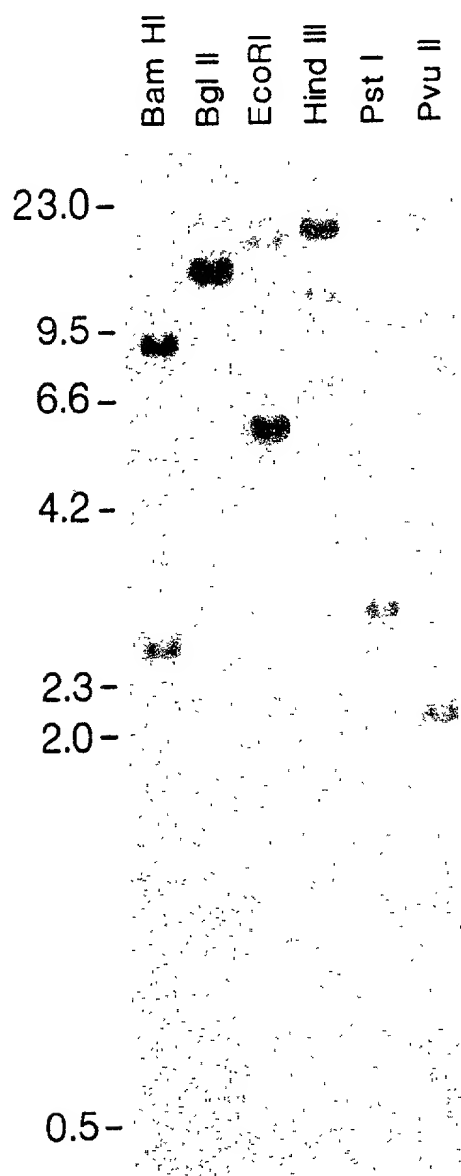
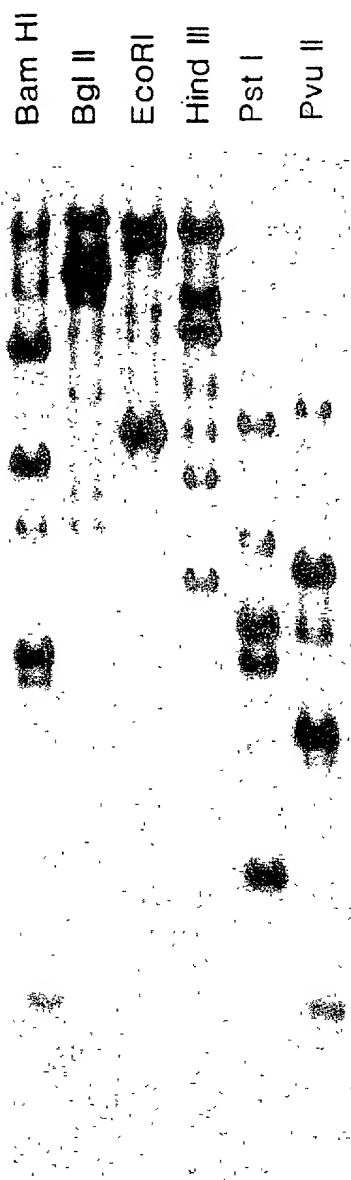


FIG. 4B



FOOTNOTES

FIG. 5

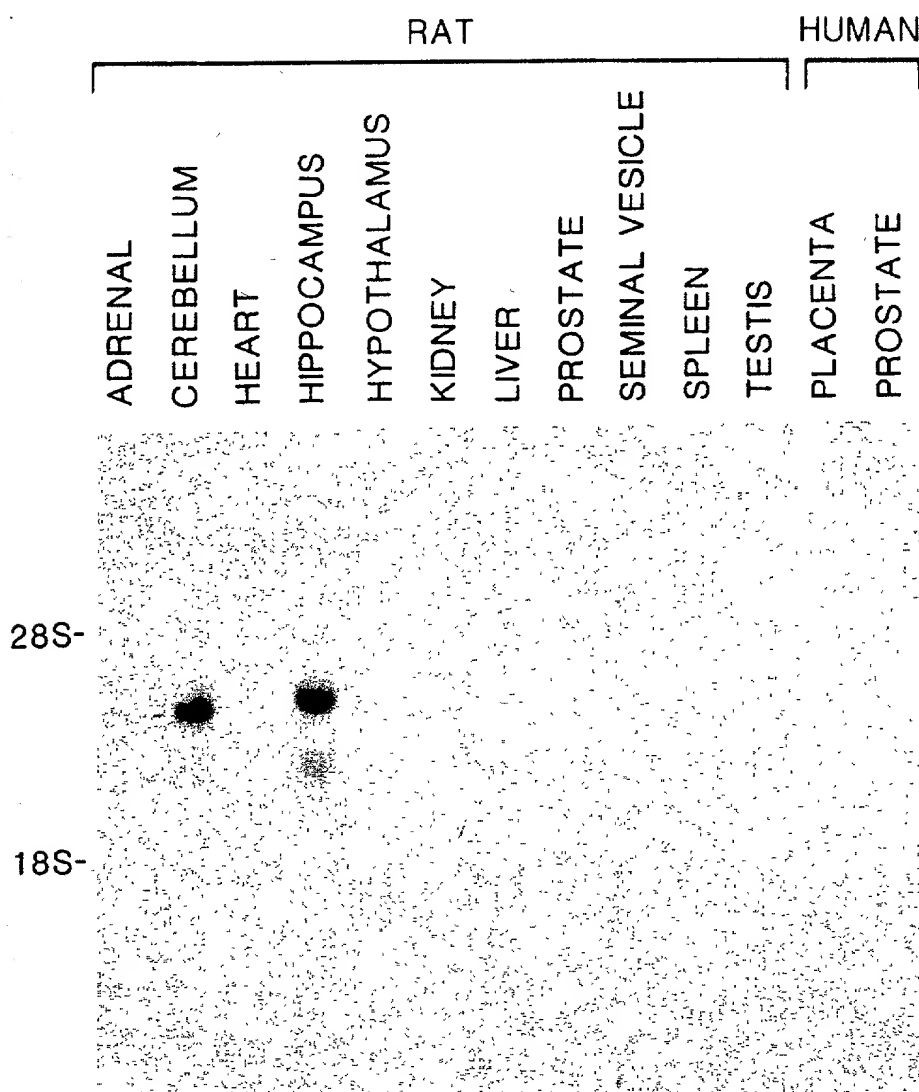


FIG. 6

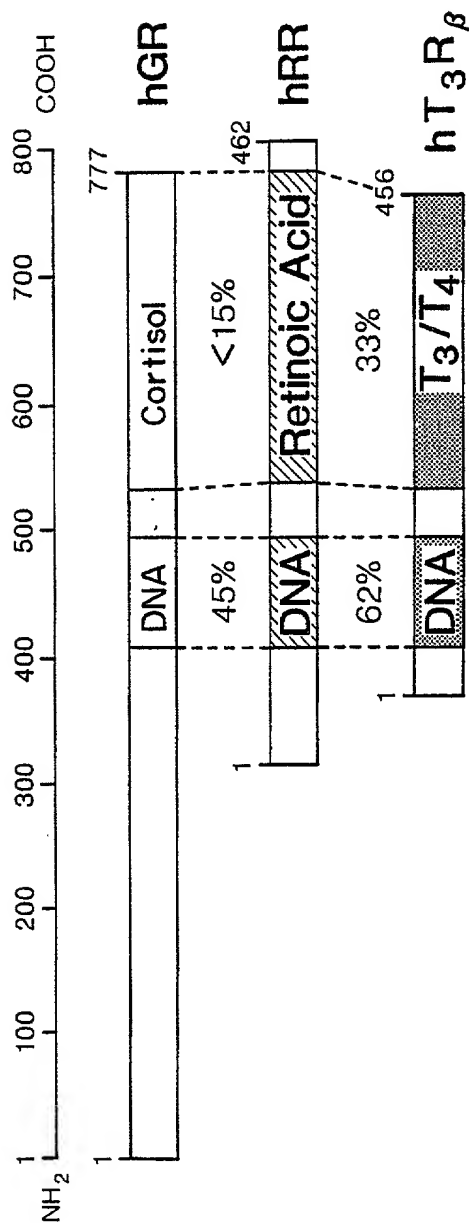


FIG. 7

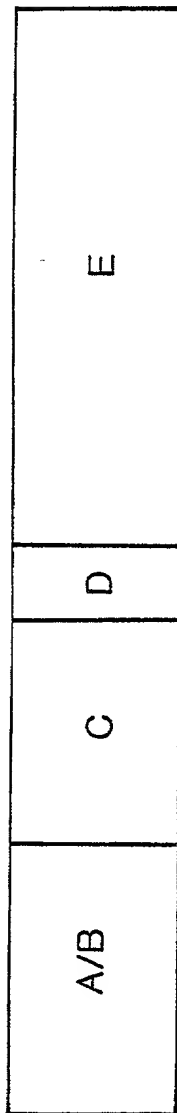
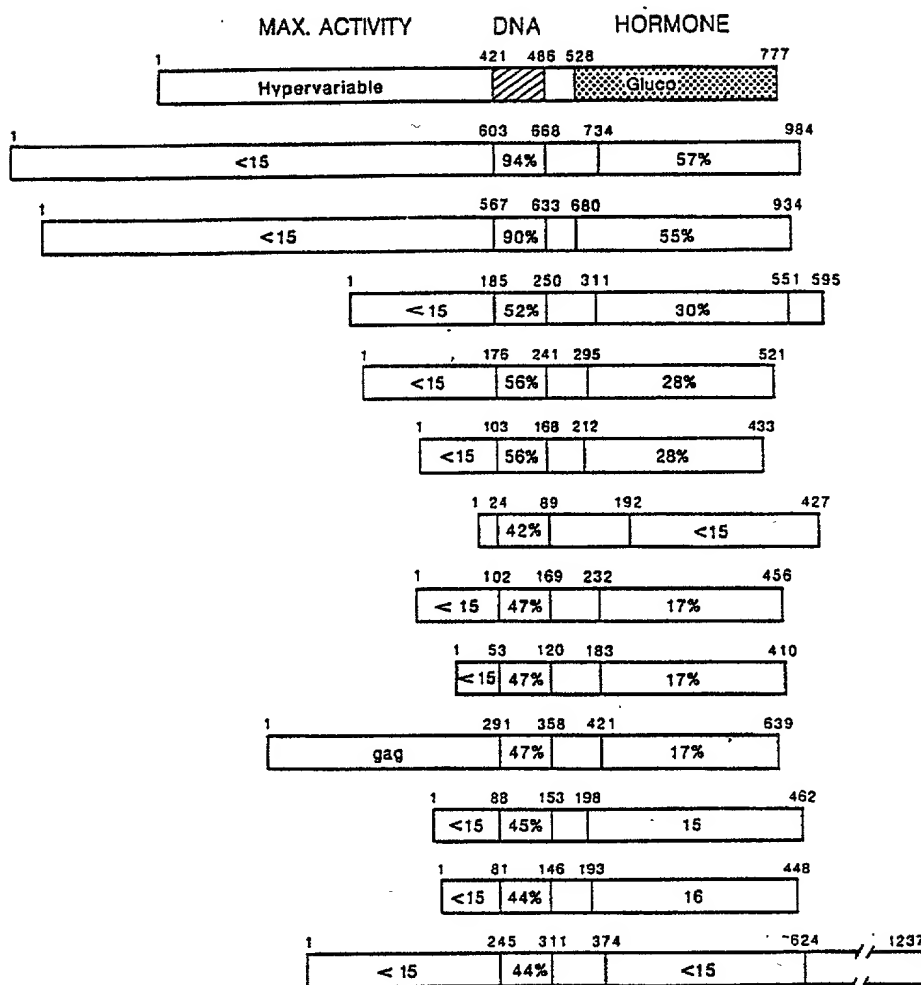


FIG. 8-1



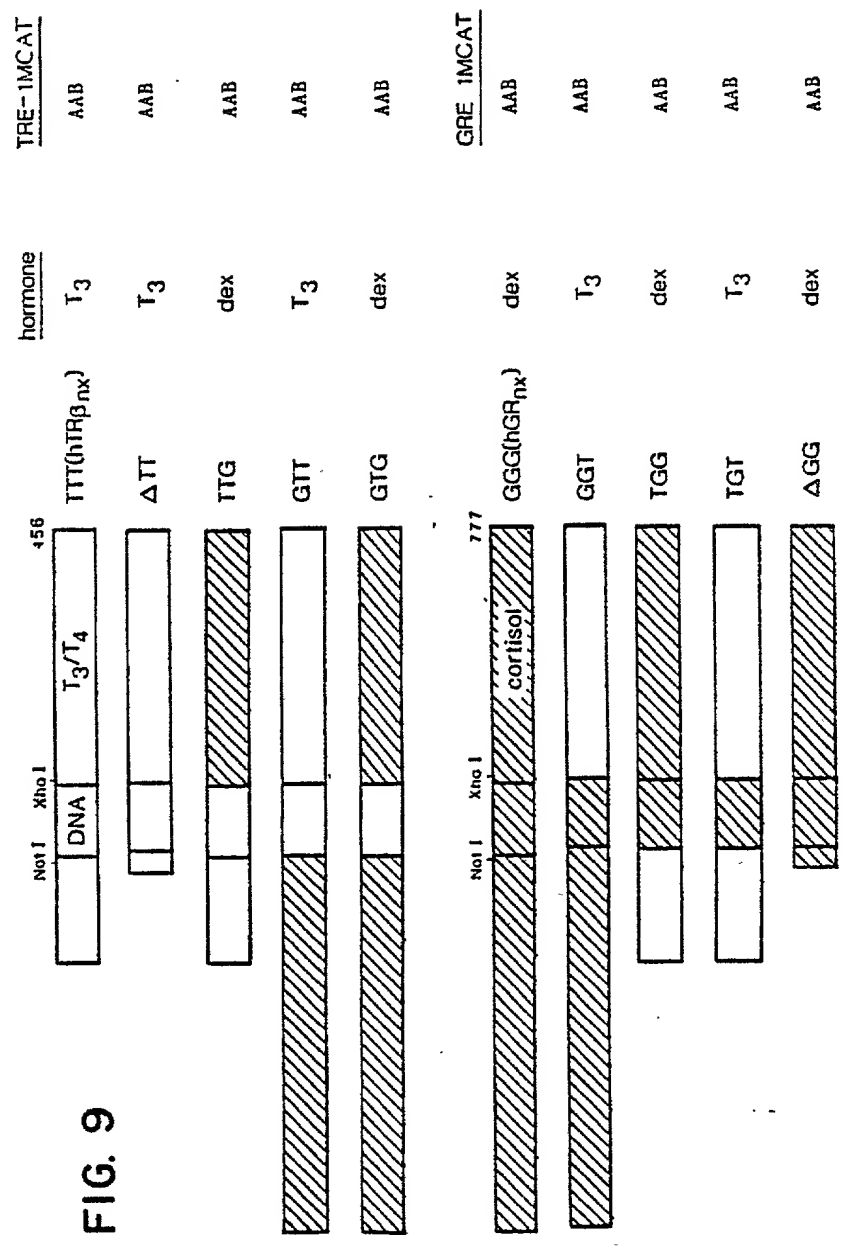
TOTAL TO 1237

FIG. 8-2

	HRE	DNA BINDING	HORMONE BINDING IN VITRO	IN VIVO	TRANS- ACTIVATION	CHROMO- SOME	SPECIES
GR	+ ¹⁵⁻¹⁹	+ ^{15,17,21}	+ ^{25,22}	+ ^{46,52, 77}	+ ^{46,52, 78,79}	5 ²⁶	h, ²⁶ r, ⁷⁷ m, ⁷⁸
MR	nd	nd	nd	+ ³⁶	+ ³⁶	4 ³⁶	h ³⁶
PR	+ ^{24,34}	+ ^{24,34}	nd	nd	+ ³⁴	11 ⁷⁹	rabbit, ³² h, ³³ c, ³⁴
ER	+ ^{22,23}	+ ^{23,52}	nd	+ ^{23,53, 62}	+ ^{53,62}	6 ⁶²	h, ²⁹ c, ³⁰ frog ³¹
ERR1	nd	nd	nd	nd	nd	nd	h ³⁹
ERR2	nd	nd	nd	nd	nd	nd	h ³⁹
VDR	nd	nd	nd	+ ³⁵	nd	nd	h, ³⁵ c ³⁵
T ₃ R _β	+ ²⁵	+ ²⁵	+ ³⁷	nd	+ ⁸⁰	3 ³⁷	h ³⁷
T ₃ R _α	nd	nd	+ ^{38,40}	nd	+ ⁸⁰	17 ⁴⁰	r, ⁴⁰ h, ⁴¹ c ³⁸
V-erb A	+	+	(-) ³⁸	nd	nd	virus	c ²⁸
RAR	nd	nd	nd	+ ^{42,43}	+ ^{42,43}	17 ⁸³	h ^{42,43}
HAP	nd	nd	nd	nd	nd	3 ⁴⁵	h ⁴⁵
E75	nd	nd	nd	nd	nd		d ⁴⁵

TOP SECRET

FIG. 9



AAB = Activation Above Background